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RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/516,338
Source: PG110
Date Processed by STIC: 12/9/04

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PCT

RAW SEQUENCE LISTING DATE: 12/09/2004
PATENT APPLICATION: US/10/516,338 **TIME:** 14:36:59

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3 <110> APPLICANT: Astex Technology Limited
4   Cosme, Jose
5   Ward, Alison
6   Vuillard, Laurent
7   Williams, Pamela
8   Hamilton, Bruce
10 <120> TITLE OF INVENTION: Methods of Purification of Cytochrome P450 Proteins
12 <130> FILE REFERENCE: AHBCP6047252
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/516,338
C--> 15 <141> CURRENT FILING DATE: 2004-11-30
17 <160> NUMBER OF SEQ ID NOS: 84
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1428
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
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27 <223> OTHER INFORMATION: Description of Artificial Sequence: 2C19 (internal
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35 ttccccactgg ctgaaagagc taacagagga tttggaatcg ttttcagccaa tgaaaaagaga 300
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37 agcattgagg accgtgttca agaggaagcc cactgccttg tggaggagtt gagaaaaaacc 420
38 aaggcttcac cctgtgatcc cactttcatc ctgggctgtg ctccctgcaat ttttgc 480
39 tccattatcc tccagaaaacg tttcgattat aaagatcagc aattttttttt ctttgatggaa 540
40 aaatttgaatg aaaacatcg gattgtaaagc acccccctggc tccagatatg caataatccc 600
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47 caggacaggg gccacatgcc ctacacagat gctgtggc acgaggtcca gagatacatc 1020
48 gacccatcc ccaccacgtt gcccctgtca gtgacccgtt acgtttttt cagaaaactac 1080
49 ctcattccca agggcacaac catattaact tccctcaactt ctgtgctaca tgacaacaaa 1140
50 gaatttccca acccagagat gtttgaccct cgtcacttgc tgcatgaagg tgaaaaatttt 1200
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 73 Lys Ser Leu Thr Asn Leu Ser Lys Ile Tyr Gly Pro Val Phe Thr Leu
 74 35 40 45
 76 Tyr Phe Gly Leu Glu Arg Met Val Val Leu His Gly Tyr Glu Val Val
 77 50 55 60
 79 Lys Glu Ala Leu Ile Asp Leu Gly Glu Glu Phe Ser Gly Arg Gly His
 80 65 70 75 80
 82 Phe Pro Leu Ala Glu Arg Ala Asn Arg Gly Phe Gly Ile Val Phe Ser
 83 85 90 95
 85 Asn Gly Lys Arg Trp Lys Glu Ile Arg Arg Phe Ser Leu Met Thr Leu
 86 100 105 110
 88 Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg Val Gln Glu
 89 115 120 125
 91 Glu Ala His Cys Leu Val Glu Glu Leu Arg Lys Thr Lys Ala Ser Pro
 92 130 135 140
 94 Cys Asp Pro Thr Phe Ile Leu Gly Cys Ala Pro Cys Asn Val Ile Cys
 95 145 150 155 160
 97 Ser Ile Ile Phe Gln Lys Arg Phe Asp Tyr Lys Asp Gln Gln Phe Leu
 98 165 170 175
 100 Asn Leu Met Glu Lys Leu Asn Glu Asn Ile Arg Ile Val Ser Thr Pro
 101 180 185 190
 103 Trp Ile Gln Ile Cys Asn Asn Phe Pro Thr Ile Ile Asp Tyr Phe Pro
 104 195 200 205
 106 Gly Thr His Asn Lys Leu Leu Lys Asn Leu Ala Phe Met Glu Ser Asp
 107 210 215 220
 109 Ile Leu Glu Lys Val Lys Glu His Gln Glu Ser Met Asp Ile Asn Asn
 110 225 230 235 240
 112 Pro Arg Asp Phe Ile Asp Cys Phe Leu Ile Lys Met Glu Lys Glu Lys
 113 245 250 255
 115 Gln Asn Gln Gln Ser Glu Phe Thr Ile Glu Asn Leu Val Ile Thr Ala
 116 260 265 270
 118 Ala Asp Leu Leu Gly Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu Arg
 119 275 280 285
 121 Tyr Ala Leu Leu Leu Leu Lys His Pro Glu Val Thr Ala Lys Val
 122 290 295 300
 124 Gln Glu Glu Ile Glu Arg Val Val Gly Arg Asn Arg Ser Pro Cys Met
 125 305 310 315 320

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130 Gln Arg Tyr Ile Asp Leu Ile Pro Thr Ser Leu Pro His Ala Val Thr
131 340 345 350
133 Cys Asp Val Lys Phe Arg Asn Tyr Leu Ile Pro Lys Gly Thr Thr Ile
134 355 360 365
136 Leu Thr Ser Leu Thr Ser Val Leu His Asp Asn Lys Glu Phe Pro Asn
137 370 375 380
139 Pro Glu Met Phe Asp Pro Arg His Phe Leu His Glu Gly Gly Asn Phe
140 385 390 395 400
142 Lys Lys Ser Asn Tyr Phe Met Pro Phe Ser Ala Gly Lys Arg Ile Cys
143 405 410 415
145 Val Gly Glu Gly Leu Ala Arg Met Glu Leu Phe Leu Phe Leu Thr Phe
146 420 425 430
148 Ile Leu Gln Asn Phe Asn Leu Lys Ser Leu Ile Asp Pro Lys Asp Leu
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164 <223> OTHER INFORMATION: Description of Artificial Sequence: 2C19 wild type
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170 atctatggcc ctgtgttac tctgtat tttt ggcctggAAC gcatgggtt gctgcattgg 180
171 tatgaagtgg tgaaggaagc cctgattgtat cttggagagg agttttctgg aagaggccat 240
172 ttcccactgg ctgaaagagc taacagagga ttttggatcg tttttagcaa tgaaagaga 300
173 tggaaaggaga tccggcggtt ctccctcatg acgctgcggaa attttggat gggaaagagg 360
174 agcattgagg accgtgttca agaggaagcc cgctgccttg tggaggagtt gagaaaaacc 420
175 aaagcttcac cctgtatcc cacttcatc ctggctgtg ctccctgcaa tgtatctgc 480
176 tccattattt tccagaaacg tttcgattat aaagatcagc aatttcttaa cttgtatggaa 540
177 aaattgaatg aaaacatcag gattgtaaac acccccttggaa tccagatatg caataatttt 600
178 cccactatca ttgattattt cccggaaacc cataacaaat tactaaaaaa cttgtctttt 660
179 atggaaagtg atatTTGGA gaaagtaaaa gaacaccaag aatcgatggaa catcaacaac 720
180 cctcgggact ttattgttg ctccctgtatc aaaatggaga aggaaaagca aaaccaacag 780
181 tctgaattca ctattgaaaaa cttggtaatc actgcagctg acttacttgg agctggaca 840
182 gagacaacaa gcacaaccct gagatatgtt ctccttctcc tgctgaagca cccagaggc 900
183 acagctaaag tccaggaaga gattgaacgt gtgtggca gaaaccggag cccctgcattg 960
184 caggacaggg gccacatgcc ctacacagat gtgtggc acgaggcca gagatacatc 1020
185 gacctcatcc ccaccagcct gccccatgca gtgacctgtg acgttaaattt cagaaactac 1080
186 ctcattccca agggcacaac catattaact tccctcaactt ctgtgctaca tgacaacaaa 1140
187 gaatttccca acccagagat gtttgaccct cgtcactttc tggatgaagg tgaaaatttt 1200
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Input Set : A:\6047252.app
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200 <223> OTHER INFORMATION: Description of Artificial Sequence: Translation of
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208     20          25          30
210 Lys Ser Leu Thr Asn Leu Ser Lys Ile Tyr Gly Pro Val Phe Thr Leu
211     35          40          45
213 Tyr Phe Gly Leu Glu Arg Met Val Val Leu His Gly Tyr Glu Val Val
214     50          55          60
216 Lys Glu Ala Leu Ile Asp Leu Gly Glu Glu Phe Ser Gly Arg Gly His
217     65          70          75          80
219 Phe Pro Leu Ala Glu Arg Ala Asn Arg Gly Phe Gly Ile Val Phe Ser
220     85          90          95
222 Asn Gly Lys Arg Trp Lys Glu Ile Arg Arg Phe Ser Leu Met Thr Leu
223     100         105         110
225 Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg Val Gln Glu
226     115         120         125
228 Glu Ala Arg Cys Leu Val Glu Glu Leu Arg Lys Thr Lys Ala Ser Pro
229     130         135         140
231 Cys Asp Pro Thr Phe Ile Leu Gly Cys Ala Pro Cys Asn Val Ile Cys
232     145         150         155         160
234 Ser Ile Ile Phe Gln Lys Arg Phe Asp Tyr Lys Asp Gln Gln Phe Leu
235     165         170         175
237 Asn Leu Met Glu Lys Leu Asn Glu Asn Ile Arg Ile Val Ser Thr Pro
238     180         185         190
240 Trp Ile Gln Ile Cys Asn Asn Phe Pro Thr Ile Ile Asp Tyr Phe Pro
241     195         200         205
243 Gly Thr His Asn Lys Leu Leu Lys Asn Leu Ala Phe Met Glu Ser Asp
244     210         215         220
246 Ile Leu Glu Lys Val Lys Glu His Gln Glu Ser Met Asp Ile Asn Asn
247     225         230         235         240
249 Pro Arg Asp Phe Ile Asp Cys Phe Leu Ile Lys Met Glu Lys Glu Lys
250     245         250         255
252 Gln Asn Gln Gln Ser Glu Phe Thr Ile Glu Asn Leu Val Ile Thr Ala
253     260         265         270
255 Ala Asp Leu Leu Gly Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu Arg
256     275         280         285
258 Tyr Ala Leu Leu Leu Leu Lys His Pro Glu Val Thr Ala Lys Val
259     290         295         300

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262 305 310 315 320
264 Gln Asp Arg Gly His Met Pro Tyr Thr Asp Ala Val Val His Glu Val
265 325 330 335
267 Gln Arg Tyr Ile Asp Leu Ile Pro Thr Ser Leu Pro His Ala Val Thr
268 340 345 350
270 Cys Asp Val Lys Phe Arg Asn Tyr Leu Ile Pro Lys Gly Thr Thr Ile
271 355 360 365
273 Leu Thr Ser Leu Thr Ser Val Leu His Asp Asn Lys Glu Phe Pro Asn
274 370 375 380
276 Pro Glu Met Phe Asp Pro Arg His Phe Leu Asp Glu Gly Gly Asn Phe
277 385 390 395 400
279 Lys Lys Ser Asn Tyr Phe Met Pro Phe Ser Ala Gly Lys Arg Ile Cys
280 405 410 415
282 Val Gly Glu Gly Leu Ala Arg Met Glu Leu Phe Leu Phe Leu Thr Phe
283 420 425 430
285 Ile Leu Gln Asn Phe Asn Leu Lys Ser Leu Ile Asp Pro Lys Asp Leu
286 435 440 445
288 Asp Thr Thr Pro Val Val Asn Gly Phe Ala Ser Val Pro Pro Phe Tyr
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291 Gln Leu Cys Phe Ile Pro Val His His His His
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296 <211> LENGTH: 1443
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298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence: 2D6 encoding
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304 <400> SEQUENCE: 5
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VERIFICATION SUMMARY
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DATE: 12/09/2004
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date